SEQUENCE LISTING

<110> Pecker, Iris

      Vlodavsky , Israel

      Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION
OF SAME IN GENETICALLY MODIFIED CELLS

<130> 27674

<160> 47

<170> PatentIn version 3.1

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tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaca    1380

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tcaccaagta cttgcggtta ccctatcctt tttctaacaa gcaagtggat aaataccttc    1500

taagaccttt gggacctcat ggattacttt ccaaatctgt ccaactcaat ggtctaactc    1560

taaagatggt ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa    1620

gttcactggg cttgccagct ttctcatata gttttttttgt gataagaaat gccaaagttg    1680

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<211> 543

<212> PRT

<213> Homo sapiens

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            20              25              30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
        35              40              45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
        50              55              60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65              70              75              80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
            85              90              95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
            100             105             110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
        115             120             125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
        130             135             140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
145             150             155             160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
                165             170             175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
            180             185             190
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Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
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Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
        210             215             220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
225             230             235             240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
            245             250             255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
            260             265             270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
        275             280             285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
    290             295             300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
305             310             315             320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
            325             330             335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
        340             345             350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
        355             360             365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
    370             375             380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385             390             395             400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
            405             410             415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
        420             425             430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
        435             440             445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
    450             455             460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465             470             475             480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
            485             490             495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
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                 500                   505                   510

    Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
            515                   520                   525


    Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
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<212> DNA

<213> Homo sapiens

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<222> (63)..(1691)

<223>

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   Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
   1               5                   10                  15

ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga    155
Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
                20                  25                  30

cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag    203
Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
            35                  40                  45

ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc    251
Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
        50                  55                  60

aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag    299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
    65                  70                  75

ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt    347
Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
80                  85                  90                  95

ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc    395
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
                100                 105                 110

ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc    443
Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
            115                 120                 125

aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa    491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
        130                 135                 140

tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag    539
Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
    145                 150                 155

ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act    587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
160                 165                 170                 175

ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta    635
Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
                180                 185                 190

tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc    683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
            195                 200                 205

ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc    731
Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
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              210                    215                    220

aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg    779
Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
        225                    230                    235

tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag    827
Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys
240                    245                    250                    255

tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct    875
Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro
                260                    265                    270

cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga    923
Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly
                275                    280                    285

gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg    971
Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg
                290                    295                    300

act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt   1019
Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe
        305                    310                    315

att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct   1067
Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro
320                    325                    330                    335

ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga   1115
Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly
                340                    345                    350

gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat   1163
Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp
                355                    360                    365

aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa   1211
Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln
                370                    375                    380

gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat   1259
Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp
        385                    390                    395

cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc   1307
Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly
400                    405                    410                    415

acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt   1355
Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu
                420                    425                    430

cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa   1403
Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu
                435                    440                    445

gga gat tta act ctg tat gcc ata aac ctc cat aac gtc acc aag tac   1451
Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr
                450                    455                    460

ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt   1499
Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu
        465                    470                    475

cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc   1547
Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu
480                    485                    490                    495

aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta   1595
Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu
                500                    505                    510

atg gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc   1643
Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe
                515                    520                    525
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tca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc    1691
Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
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<212>  DNA

<213>  Mus musculus


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tccactgcac taacgtctat cacccacgat atcaggaagg agatctaact ctgtatgtcc    360

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ctctccccgc aggaagtgca ctaagcctgc ctgccttttc ctatggtttt tttgtcataa    600

gaaatgccaa aatcgctgct tgtatatgaa aataaaaggc atacggtacc cctgagacaa    660

aagccgaggg gggtgttatt cataaaacaa aaccctagtt taggaggcca cctccttgcc    720

gagttccaga gcttcgggag ggtggggtac acttcagtat tacattcagt gtggtgttct    780

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<213>  Homo sapiens


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aggcgtaacg gggcggagga aaggagaaaa gggcgctggg gctcggcggg aggaagtgct    180

agagctctcg actctccgct cgcggcagc tggcgggggg agcagccagg tgagcccaag     240

atgctgctgc gctcgaagcc tgcgctgccg ccgccgctga tgctgctgct cctggggccg    300

ctgggtcccc tctccccctgg cgccctgccc cgacctgcgc aagcacagga cgtcgtggac    360

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attgacgcca acctggccac ggacccgcgg ttcctcatcc tcctgggttc tccaaagctt    480

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caagtcaacc aggatatttg caaatatgga tccatccctc ctgatgtgga ggagaagtta      660

cggttggaat ggccctacca ggagcaattg ctactccgag aacactacca gaaaaagttc      720

aagaacagca cctactcaag aagctctgta gatgtgctat acacttttgc aaactgctca      780

ggactggact tgatctttgg cctaaatgcg ttattaagaa cagcagattt gcagtggaac      840

agttctaatg ctcagttgct cctggactac tgctcttcca aggggtataa catttcttgg      900

gaactaggca atgaacctaa cagtttcctt aagaaggctg atattttcat caatgggtcg      960

cagttaggag aagattatat tcaattgcat aaacttctaa gaaagtccac cttcaaaaat     1020

gcaaaactct atggtcctga tgttggtcag cctcgaagaa agacggctaa gatgctgaag     1080

agcttcctga aggctggtgg agaagtgatt gattcagtta catggcatca ctactatttg     1140

aatggacgga ctgctaccag ggaagatttt ctaaaccctg atgtattgga cattttattt     1200

tcatctgtgc aaaaagtttt ccaggtggtt gagagcacca ggcctggcaa gaaggtctgg     1260

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accaagtact tgcggttacc ctatcctttt tctaacaagc aagtggataa ataccttcta      1680

agacctttgg gacctcatgg attactttcc aaatctgtcc aactcaatgg tctaactcta     1740

aagatggtgg atgatcaaac cttgccacct ttaatggaaa aacctctccg gccaggaagt     1800

tcactgggct tgccagcttt ctcatatagt ttttttgtga taagaaatgc caaagttgct     1860

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<211> 592

<212> PRT

<213> Homo sapiens

<400> 14

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            20                  25                  30


Asp Ser Pro Leu Arg Gly Ser Trp Arg Gly Glu Gln Pro Gly Glu Pro
        35                  40                  45


Lys Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
    50                  55                  60
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```
Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
65            70            75            80

Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
            85            90            95

Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
            100           105           110

Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
            115           120           125

Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
            130           135           140

Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
145           150           155           160

Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
            165           170           175

Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
            180           185           190

Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
            195           200           205

Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
210           215           220

Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
225           230           235           240

Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
            245           250           255

Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
            260           265           270

Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
            275           280           285

Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys
            290           295           300

Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro
305           310           315           320

Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly
            325           330           335

Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg
            340           345           350

Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe
            355           360           365

Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro
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                    370                 375                 380

        Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly
        385                 390                 395                 400

        Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp
                            405                 410                 415

        Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln
                            420                 425                 430

        Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp
                    435                 440                 445

        Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly
            450                 455                 460

        Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu
        465                 470                 475                 480

        Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu
                        485                 490                 495

        Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr
                    500                 505                 510

        Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu
                515                 520                 525

        Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu
            530                 535                 540

        Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu
        545                 550                 555                 560

        Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe
                    565                 570                 575

        Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
                    580                 585                 590
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<210> 15

<211> 1899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94)..(1869)

<223>

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cagtgggagg gatgcagaag aggagtggga ggg atg gag ggc gca gtg gga ggg    114
                                        Met Glu Gly Ala Val Gly Gly
                                        1                   5

gtg agg agg cgt aac ggg gcg gag gaa agg aga aaa ggg cgc tgg ggc      162
Val Arg Arg Arg Asn Gly Ala Glu Glu Arg Arg Lys Gly Arg Trp Gly
        10                  15                  20

tcg gcg gga gga agt gct aga gct ctc gac tct ccg ctg cgc ggc agc      210
Ser Ala Gly Gly Ser Ala Arg Ala Leu Asp Ser Pro Leu Arg Gly Ser
    25                  30                  35

tgg cgg ggg gag cag cca ggt gag ccc aag atg ctg ctg cgc tcg aag      258
Trp Arg Gly Glu Gln Pro Gly Glu Pro Lys Met Leu Leu Arg Ser Lys
40                  45                  50                  55

cct gcg ctg ccg ccg ccg ctg atg ctg ctg ctc ctg ggg ccg ctg ggt      306
Pro Ala Leu Pro Pro Pro Leu Met Leu Leu Leu Gly Pro Leu Gly
                60                  65                  70

ccc ctc tcc cct ggc gcc ctg ccc cga cct gcg caa gca cag gac gtc      354
Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro Ala Gln Ala Gln Asp Val
            75                  80                  85

gtg gac ctg gac ttc ttc acc cag gag ccg ctg cac ctg gtg agc ccc      402
Val Asp Leu Asp Phe Phe Thr Gln Glu Pro Leu His Leu Val Ser Pro
        90                  95                  100

tcg ttc ctg tcc gtc acc att gac gcc aac ctg gcc acg gac ccg cgg      450
Ser Phe Leu Ser Val Thr Ile Asp Ala Asn Leu Ala Thr Asp Pro Arg
    105                 110                 115

ttc ctc atc ctc ctg ggt tct cca aag ctt cgt acc ttg gcc aga ggc      498
Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr Leu Ala Arg Gly
120                 125                 130                 135

ttg tct cct gcg tac ctg agg ttt ggt ggc acc aag aca gac ttc cta      546
Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu
                140                 145                 150

att ttc gat ccc aag aag gaa tca acc ttt gaa gag aga agt tac tgg      594
Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe Glu Glu Arg Ser Tyr Trp
            155                 160                 165

caa tct caa gtc aac cag gat att tgc aaa tat gga tcc atc cct cct      642
Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly Ser Ile Pro Pro
        170                 175                 180

gat gtg gag gag aag tta cgg ttg gaa tgg ccc tac cag gag caa ttg      690
Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr Gln Glu Gln Leu
    185                 190                 195

cta ctc cga gaa cac tac cag aaa aag ttc aag aac agc acc tac tca      738
Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys Asn Ser Thr Tyr Ser
200                 205                 210                 215

aga agc tct gta gat gtg cta tac act ttt gca aac tgc tca gga ctg      786
Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser Gly Leu
                220                 225                 230

gac ttg atc ttt ggc cta aat gcg tta tta aga aca gca gat ttg cag      834
Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp Leu Gln
                235                 240                 245

tgg aac agt tct aat gct cag ttg ctc ctg gac tac tgc tct tcc aag      882
Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys
            250                 255                 260

ggg tat aac att tct tgg gaa cta ggc aat gaa cct aac agt ttc ctt      930
Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Leu
    265                 270                 275

aag aag gct gat att ttc atc aat ggg tcg cag tta gga gaa gat tat      978
Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly Glu Asp Tyr
280                 285                 290                 295
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att caa ttg cat aaa ctt cta aga aag tcc acc ttc aaa aat gca aaa      1026
Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys
            300             305             310

ctc tat ggt cct gat gtt ggt cag cct cga aga aag acg gct aag atg      1074
Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys Met
            315             320             325

ctg aag agc ttc ctg aag gct ggt gga gaa gtg att gat tca gtt aca      1122
Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val Thr
            330             335             340

tgg cat cac tac tat ttg aat gga cgg act gct acc agg gaa gat ttt      1170
Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp Phe
            345             350             355

cta aac cct gat gta ttg gac att ttt att tca tct gtg caa aaa gtt      1218
Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val
360             365             370             375

ttc cag gtg gtt gag agc acc agg cct ggc aag aag gtc tgg tta gga      1266
Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu Gly
            380             385             390

gaa aca agc tct gca tat gga ggc gga gcg ccc ttg cta tcc gac acc      1314
Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asp Thr
            395             400             405

ttt gca gct ggc ttt atg tgg ctg gat aaa ttg ggc ctg tca gcc cga      1362
Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Arg
            410             415             420

atg gga ata gaa gtg gtg atg agg caa gta ttc ttt gga gca gga aac      1410
Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn
            425             430             435

tac cat tta gtg gat gaa aac ttc gat cct tta cct gat tat tgg cta      1458
Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu Pro Asp Tyr Trp Leu
440             445             450             455

tct ctt ctg ttc aag aaa ttg gtg ggc acc aag gtg tta atg gca agc      1506
Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys Val Leu Met Ala Ser
            460             465             470

gtg caa ggt tca aag aga agg aag ctt cga gta tac ctt cat tgc aca      1554
Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val Tyr Leu His Cys Thr
            475             480             485

aac act gac aat cca agg tat aaa gaa gga gat tta act ctg tat gcc      1602
Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp Leu Thr Leu Tyr Ala
            490             495             500

ata aac ctc cat aac gtc acc aag tac ttg cgg tta ccc tat cct ttt      1650
Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg Leu Pro Tyr Pro Phe
505             510             515

tct aac aag caa gtg gat aaa tac ctt cta aga cct ttg gga cct cat      1698
Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg Pro Leu Gly Pro His
520             525             530             535

gga tta ctt tcc aaa tct gtc caa ctc aat ggt cta act cta aag atg      1746
Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met
            540             545             550

gtg gat gat caa acc ttg cca cct tta atg gaa aaa cct ctc cgg cca      1794
Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg Pro
            555             560             565

gga agt tca ctg ggc ttg cca gct ttc tca tat agt ttt ttt gtg ata      1842
Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val Ile
            570             575             580

aga aat gcc aaa gtt gct gct tgc atc tgaaaataaa atatactagt            1889
Arg Asn Ala Lys Val Ala Ala Cys Ile
            585             590

cctgacactg                                                           1899
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<211> 594

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<213> Homo sapiens

<400> 16

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tttttcagg caaaagtaaa atacctgaga aactgcctgg ccagaggaca atcagatttt      180

ggctggctca agtgacaagc aagtgtttat aagctagatg ggagaggaag ggatgaatac     240

tccattggag gctttactcg agggtcagag ggatacccgg cgccatcaga atgggatctg     300

ggagtcggaa acgctgggtt cccacgagag cgcgcagaac acgtgcgtca ggaagcctgg     360

tccgggatgc ccagcgctgc tccccgggcg ctcctccccg ggcgctcctc cccaggcctc     420

ccgggcgctt ggatcccggc catctccgca cccttcaagt gggtgtgggt gatttcgtaa     480

gtgaacgtga ccgccaccgg ggggaaagcg agcaaggaag taggagagag ccgggcaggc     540

ggggcggggt tggattggga gcagtgggag ggatgcagaa gaggagtggg aggg           594
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<210> 17

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<211> 21

<212> PRT

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<220>

<223> Synthetic oligonucleotide

<400> 18

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Ala Gly Cys Ala Thr
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<213>  Artificial sequence


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<223>  Synthetic oligonucleotide
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<210>  20

<211>  19

<212>  DNA

<213>  Artificial sequence


<220>

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<210>  21

<211>  21

<212>  DNA

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<223>  Synthetic oligonucleotide
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cttgggctca cctggctgct c                                           21


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<400> 28
gcatcttagc cgtctttctt cg   22

<210> 29

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gtagtgatgc catgtaactg aatc   24

<210> 30

<211> 22

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<400> 30
aggcacccta gagatgttcc ag   22

<210> 31

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide

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<210>  32

<211>  25

<212>  DNA

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<220>

<223>  Synthetic oligonucleotide

<400>  32
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<210>  33

<211>  22

<212>  DNA

<213>  Artificial sequence



<220>

<223>  Synthetic oligonucleotide

<400>  33
cgaagctctg gaactcggca ag                                      22


<210>  34

<211>  22

<212>  DNA

<213>  Artificial sequence



<220>

<223>  Synthetic oligonucleotide

<400>  34
gccagctgca aggtgttgg ac                                       22


<210>  35

<211>  23

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<220>

<223>  Synthetic oligonucleotide

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<210>  36

<211>  22

<212>  DNA

<213>  Artificial sequence


<220>

<223>  Synthetic oligonucleotide

<400>  36
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<210>  37

<211>  22

<212>  DNA

<213>  Artificial sequence


<220>

<223>  Synthetic oligonucleotide

<400>  37
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<210>  38

<211>  22

<212>  DNA

<213>  Artificial sequence


<220>

<223>  Synthetic oligonucleotide

<400>  38
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<210>  39

<211>  19

<212>  DNA

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<400>  39
actatagggc acgcgtggt                                                  19


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<212> DNA

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<400> 40
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<210> 41

<211> 23

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<400> 41
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<210> 42

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<212> DNA

<213> Homo sapiens

<400> 42

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ttgaactctt gggctctagt gatccacccg ccttggcctc ccaaagtgct gggattacag     180

gtgtgagcca tcacacccgg ccccccgttt ccatattagt aactcacatg tagaccacaa     240

ggatgcacta tttagaaaac ttgcaatggt ccacttttca aatcacccaa acatgttaaa     300

gaaattggta tgactgggca tggcacagtg gctcatgcct gcaatcctag cattttgtga     360

ggctgagacg ggcagatcac gaggtcagga gattgagacc atcctgacag acatggtgaa     420

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aaaaaaaaaa aaagaaagaa attggtatga ctgttgactc acaacaggag tcagggcat     660

ggggtggggt gtaagattaa tgtcatgaca aatgtggaaa agaaacttct gttttccaa     720

ctccacgtct gctaccatat tattacactc ttctggtagt gtggtgttta tgtgtgaatt     780

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tatgagctta gctttttaagt tgcttaagaa taggtagatc tatgcaaata atgataatta     900

ttattattat tttaagagag ggtctcactt tgtcacccag gctggagtgc agtggtgtga     960

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cagtagctgg aaccacaggc acgggccacc acgcctggct aattttttgt attttttgta   1080

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accatgcctg gcctgattta tgcaaattag atatgcattt caaaataatc tatttttatt   1260

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cttactcaac caatatttat tagactctta ctaagcacca acatgatcac atgcctgagc   1380

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tcctcacctt cctgggctct ccaaggctcc gtgctctggc tagaggctta tctcctgcat     840

acttgagatt tggcggcaca aagactgact tccttatttt tgatccggac aaggaaccga     900

cttccgaaga aagaagttac tggaaatctc aagtcaacca tgatatttgc aggtctgagc     960

cggtctctgc tgcggtgttg aggaaactcc aggtggaatg ccccttccag gagctgttgc    1020

tgctccgaga gcagtaccaa aaggagttca agaacagcac ctactcaaga agctcagtgg    1080

acatgctcta cagttttgcc aagtgctcgg ggttagacct gatctttggt ctaaatgcgt    1140

tactacgaac cccagactta cggtggaaca gctccaacgc ccagcttctc cttgactact    1200

gctcttccaa gggttataac atctcctggg aactgggcaa tgagcccaac agtttctgga    1260

agaaagctca cattctcatc gatgggttgc agttaggaga agactttgtg gagttgcata    1320

aacttctaca aaggtcagct ttccaaaatg caaaactcta tggtcctgac atcggtcagc    1380

ctcgagggaa gacagttaaa ctgctgagga gtttcctgaa ggctggcgga gaagtgatcg    1440

actctcttac atggcatcac tattacttga atggacgcat cgctaccaaa gaagattttc    1500

tgagctctga tgcgctggac acttttattc tctctgtgca aaaaattctg aaggtcacta    1560

aagagatcac acctggcaag aaggtctggt tgggagagac gagctcagct tacggtggcg    1620

gtgcacccct tgctgtccaa acctttgcag ctggctttat gtggctggat aaattgggcc    1680

tgtcagccca gatgggcata gaagtcgtga tgaggcaggt gttcttcgga gcaggcaact    1740

accacttagt ggatgaaaac tttgagcctt tacctgatta ctggctctct cttctgttca    1800

agaaactggt aggtcccagg gtgttactgt caagagtgaa aggcccagac aggagcaaac    1860

tccgagtgta tctccactgc actaacgtct atcacccacg atatcaggaa ggagatctaa    1920

ctctgtatgt cctgaacctc cataatgtca ccaagcactt gaaggtaccg cctccgttgt    1980
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tcaggaaacc agtggatacg taccttctga agccttcggg gccggatgga ttactttcca   2040

aatctgtcca actgaacggt caaattctga agatggtgga tgagcagacc ctgccagctt   2100

tgacagaaaa acctctcccc gcaggaagtg cactaagcct gcctgccttt tcctatggtt   2160

tttttgtcat aagaaatgcc aaaatcgctg cttgtatatg aaaataaaag gcatacggta   2220

cccctgagac aaaagccgag gggggtgtta ttcataaaac aaaaccctag tttaggaggc   2280

cacctccttg ccgagttcca gagcttcggg agggtggggt acacttcagt attacattca   2340

gtgtggtgtt ctctctaaga agaatactgc aggtggtgac agttaatagc actgtg       2396
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<210> 44

<211> 535

<212> PRT

<213> Mus musculus

<400> 44

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Ala Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val Val Asp
            20                  25                  30


Leu Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser Pro Ser Phe
        35                  40                  45


Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu
    50                  55                  60


Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser
65                  70                  75                  80


Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe
                85                  90                  95


Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser
            100                 105                 110


Gln Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val
        115                 120                 125


Leu Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu
    130                 135                 140


Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser
145                 150                 155                 160


Ser Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu
                165                 170                 175


Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn
            180                 185                 190


Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr
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                    195                 200                 205


Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys
    210                 215                 220


Ala His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu
225                 230                 235                 240


Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr
                245                 250                 255


Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg
                260                 265                 270


Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His
            275                 280                 285


His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser
    290                 295                 300


Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys
305                 310                 315                 320


Val Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr
                325                 330                 335


Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala
            340                 345                 350


Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly
        355                 360                 365


Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His
    370                 375                 380


Leu Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu
385                 390                 395                 400


Leu Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys
            405                 410                 415


Gly Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val
            420                 425                 430


Tyr His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn
        435                 440                 445


Leu His Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg
    450                 455                 460


Lys Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu
465                 470                 475                 480


Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp
            485                 490                 495


Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser
            500                 505                 510
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     Ala Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn
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     Ala Lys Ile Ala Ala Cys Ile
         530                 535


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<211>  2396

<212>  DNA

<213>  Mus musculus


<220>

<221>  CDS

<222>  (594)..(2198)

<223>


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ttaaggcaga agggagtcgg ggtagggtct ggctgaaccc tcaaccgggg cttttaactc     180

agggtctagt cctggcgcca aatggatggg acctagaaaa ggtgacagag tgcgcaggac     240

accaggaagc tggtcccacc cctgcgcggc tcccgggcgc tccctcccca ggcctccgag     300

gatcttggat tctggccacc tccgcaccct ttggatgggt gtggatgatt tcaaaagtgg     360

acgtgaccgc ggcggagggg aaagccagca cggaaatgaa agagagcgag gaggggaggg     420

cggggagggg aggcgctag ggagggactc ccggagggg tgggagggat ggagcgctgt       480

gggagggtac tgagtcctgg cgccagaggc gaagcaggac cggttgcagg gggcttgagc     540

cagcgcgccg gctgccccag ctctcccggc agcgggcggt ccagccaggt ggg atg       596
                                                              Met
                                                              1

ctg agg ctg ctg ctg ctg tgg ctc tgg ggg ccg ctc ggt gcc ctg gcc     644
Leu Arg Leu Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala Leu Ala
            5                  10                  15

cag ggc gcc ccc gcg ggg acc gcg ccg acc gac gac gtg gta gac ttg     692
Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val Val Asp Leu
        20                  25                  30

gag ttt tac acc aag cgg ccg ctc cga agc gtg agt ccc tcg ttc ctg     740
Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser Pro Ser Phe Leu
    35                  40                  45

tcc atc acc atc gac gcc agc ctg gcc acc gac ccg cgc ttc ctc acc     788
Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu Thr
50                  55                  60                  65

ttc ctg ggc tct cca agg ctc cgt gct ctg gct aga ggc tta tct cct     836
Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser Pro
                70                  75                  80

gca tac ttg aga ttt ggc ggc aca aag act gac ttc ctt att ttt gat     884
Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp
            85                  90                  95
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ccg gac aag gaa ccg act tcc gaa gaa aga agt tac tgg aaa tct caa       932
Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser Gln
        100                     105                 110

gtc aac cat gat att tgc agg tct gag ccg gtc tct gct gcg gtg ttg       980
Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val Leu
        115                     120                 125

agg aaa ctc cag gtg gaa tgg ccc ttc cag gag ctg ttg ctg ctc cga      1028
Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg
130                     135                 140                 145

gag cag tac caa aag gag ttc aag aac agc acc tac tca aga agc tca      1076
Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser
                150                     155                 160

gtg gac atg ctc tac agt ttt gcc aag tgc tcg ggg tta gac ctg atc      1124
Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile
                165                     170                 175

ttt ggt cta aat gcg tta cta cga acc cca gac tta cgg tgg aac agc      1172
Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser
                180                     185                 190

tcc aac gcc cag ctt ctc ctt gac tac tgc tct tcc aag ggt tat aac      1220
Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn
        195                     200                 205

atc tcc tgg gaa ctg ggc aat gag ccc aac agt ttc tgg aag aaa gct      1268
Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala
210                     215                 220                 225

cac att ctc atc gat ggg ttg cag tta gga gaa gac ttt gtg gag ttg      1316
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu Leu
                230                     235                 240

cat aaa ctt cta caa agg tca gct ttc caa aat gca aaa ctc tat ggt      1364
His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr Gly
                245                     250                 255

cct gac atc ggt cag cct cga ggg aag aca gtt aaa ctg ctg agg agt      1412
Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg Ser
                260                     265                 270

ttc ctg aag gct ggc gga gaa gtg atc gac tct ctt aca tgg cat cac      1460
Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His His
        275                     280                 285

tat tac ttg aat gga cgc atc gct acc aaa gaa gat ttt ctg agc tct      1508
Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser Ser
290                     295                 300                 305

gat gcg ctg gac act ttt att ctc tct gtg caa aaa att ctg aag gtc      1556
Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys Val
                310                     315                 320

act aaa gag atc aca cct ggc aag aag gtc tgg ttg gga gag acg agc      1604
Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser
                325                     330                 335

tca gct tac ggt ggc ggt gca ccc ttg ctg tcc aac acc ttt gca gct      1652
Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala Ala
                340                     345                 350

ggc ttt atg tgg ctg gat aaa ttg ggc ctg tca gcc cag atg ggc ata      1700
Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly Ile
        355                     360                 365

gaa gtc gtg atg agg cag gtg ttc ttc gga gca ggc aac tac cac tta      1748
Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu
370                     375                 380                 385

gtg gat gaa aac ttt gag cct tta cct gat tac tgg ctc tct ctt ctg      1796
Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu
                390                     395                 400

ttc aag aaa ctg gta ggt ccc agg gtg tta ctg tca aga gtg aaa ggc      1844
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Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly
            405                 410                 415

cca gac agg agc aaa ctc cga gtg tat ctc cac tgc act aac gtc tat      1892
Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr
            420                 425                 430

cac cca cga tat cag gaa gga gat cta act ctg tat gtc ctg aac ctc      1940
His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu
        435                 440                 445

cat aat gtc acc aag cac ttg aag gta ccg cct ccg ttg ttc agg aaa      1988
His Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys
450                 455                 460                 465

cca gtg gat acg tac ctt ctg aag cct tcg ggg ccg gat gga tta ctt      2036
Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu Leu
                470                 475                 480

tcc aaa tct gtc caa ctg aac ggt caa att ctg aag atg gtg gat gag      2084
Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp Glu
            485                 490                 495

cag acc ctg cca gct ttg aca gaa aaa cct ctc ccc gca gga agt gca      2132
Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser Ala
            500                 505                 510

cta agc ctg cct gcc ttt tcc tat ggt ttt ttt gtc ata aga aat gcc      2180
Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn Ala
        515                 520                 525

aaa atc gct gct tgt ata tgaaaataaa aggcatacgg tacccctgag            2228
Lys Ile Ala Ala Cys Ile
530                 535

acaaaagccg aggggggtgt tattcataaa acaaaaccct agtttaggag gccacctcct    2288

tgccgagttc cagagcttcg ggagggtggg gtacacttca gtattacatt cagtgtggtg    2348

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<211> 385

<212> DNA

<213> Rattus norvegicus

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cggttcctca ccttcctgag ctctccacgg cttcgagccc tgtctagagg cttatctcct    240

gcgtacttga gatttggcgg caccaagact gacttcctta tttttgatcc caacaacgaa    300

cccacctctg aagaaagaag ttactggcaa tctcaagaca acaatgatat ttgcgggtct    360

gaccgggtct ccgctgacgt gttga                                          385
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<210> 47

<211> 541

<212> DNA

<213> Rattus norvegicus

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<222> (507)..(507)

<223> Any nucleotide

<400> 47

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cattaactgt caccacctgc agtggtctac ttagagaaca ccgcactgga tgttaacact       180

gaagcgcgtg ccccgccctc ccgaggctct ggatccagcg ttgaagcttg ccccgccctc       240

ccgaggctct ggatccagca ctggagcatg ccccgccctc ccgaggctct ggagcttgct       300

aaggagtccg ctccctaccg ctggggtttt gctttattct tatgaatgac acccctgacc       360

gctttcgtct caggggtact gtaatgcctt ttattttcat atacaagctg cgattttggc       420

atttcttatg acaaaaaacc cataggaaaa ggcgggcacg cttagtgagc ttcctgcggg       480

gagaggtttt tctgttagag ctggcanggt ctgctcatcg accatcttca ggcctcgtgc       540

c                                                                      541
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